Amendments to the Specification

Please replace the paragraph beginning at page 10, line 27, with the following amended paragraph.

Figures 9A-9C show tables of information for use in describing one example of the use of an analysis process according to the present invention. The sequence identification numbers for motif numbers 1-12 are as follows: motif number 1, SEQ ID NO:6; motif number 2, SEQ ID NO:7; motif number 3, SEQ ID NO:8; motif number 4, SEQ ID NO:9; motif number 5, SEQ ID NO:10; motif number 6, SEQ ID NO:11; motif number 7, SEQ ID NO:12; motif number 8, SEQ ID NO:13; motif number 9, SEQ ID NO:14; motif number 10, SEQ ID NO:15; motif number 11, SEQ ID NO:16; motif number 12, SEQ ID NO:17.

Please replace the paragraph beginning at page 18, line 2, with the following amended paragraph.

Databases that have been assembled with expert user knowledge, such as the PROSITE database (~~http://~~ available at the website us.expasy.org/prosite/), which is a summary of data that may occur in other databases as well, is a list of motifs that have been defined as specific for a protein family. The syntax of the motif data storage system is limited to those specifically defined by the expert defining the motifs. The motifs are not automatically derived and are described in alphabetic fashion, and not according to physical chemical properties as in the method described according to the present invention.

Please replace the paragraph beginning at page 18, line 9, with the following amended paragraph.

The motifs defined by the E-motif program (~~http://~~ available at the website fold.stanford.edu~~/emotif/emotif-maker.html~~) are automatically derived but are not defined according to aggregate physical chemical properties in a systematic fashion such as that described according to the present invention. The approach to sequence database searching is different and less systematic than that according to the present invention. Neither the E-motif nor the PROSITE approach seeks to link structural data to further define motifs in the form of molegos, conserved units in protein families that are conserved in both structure and sequence.